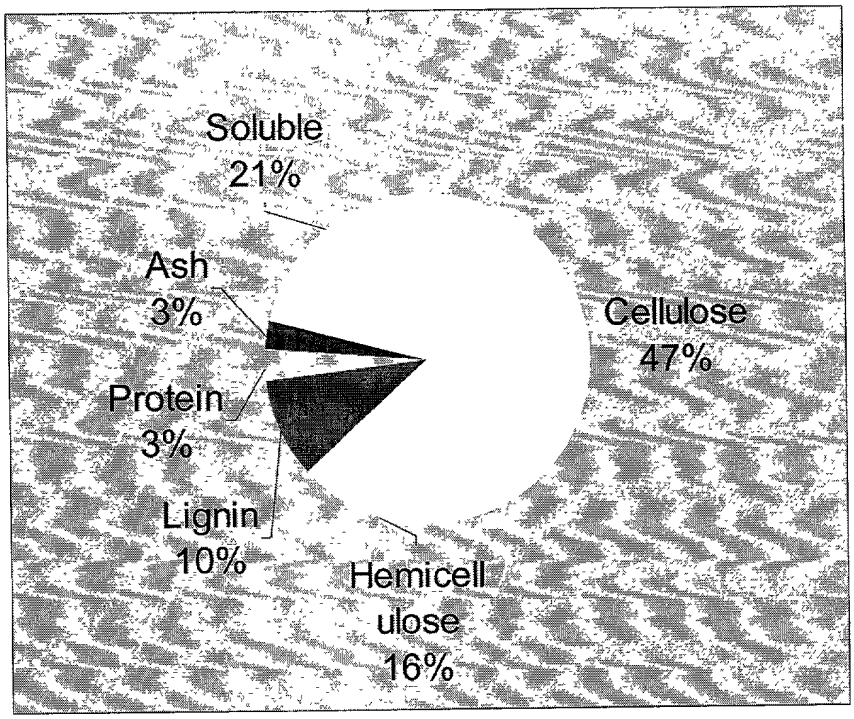



**Figure 1.**

Document #: 2004204

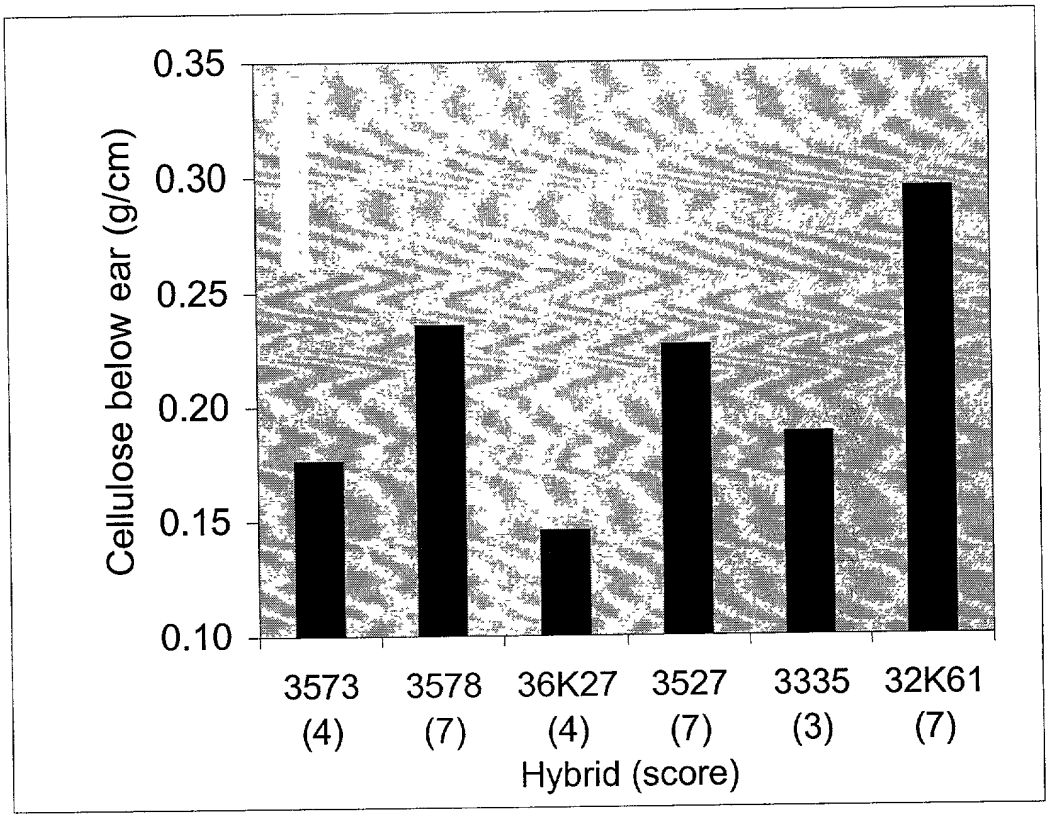

0.35
0.30
0.25
0.20
0.15
0.10
Cellulose below ear (g/cm)
3573 (4)
3578 (7)
36K27 (4)
3527 (7)
3335 (3)
32K61 (7)
Hybrid (score)

**Figure 2**

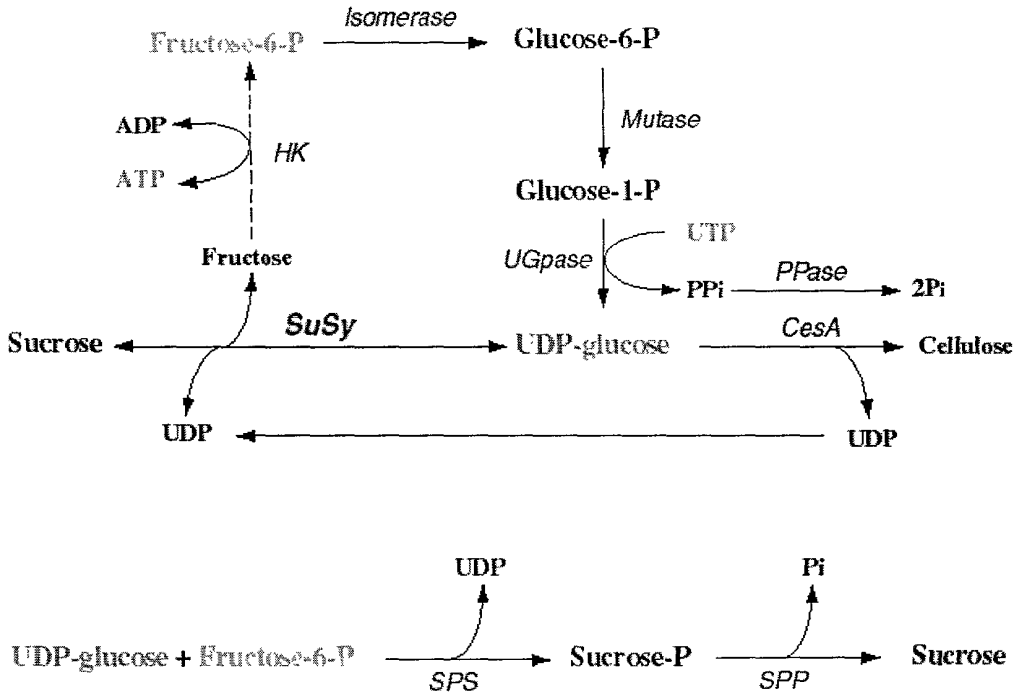






**Figure 3.**

2010 Feb 24 00:00:00

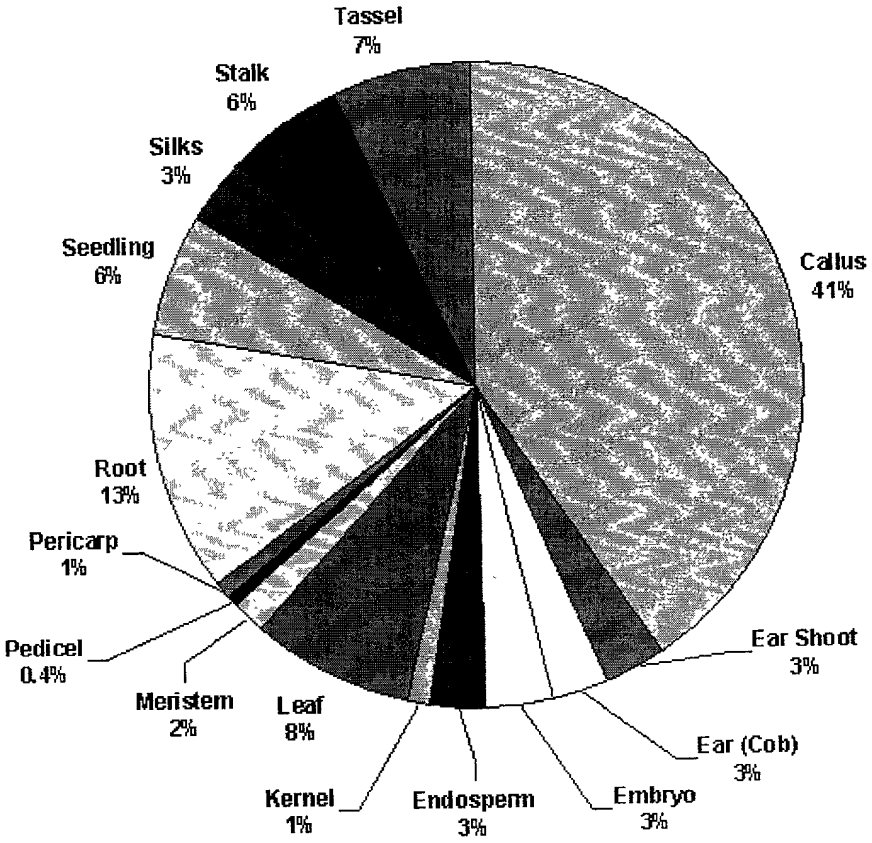

Tassel
7%
Stalk
6%
Silks
3%
Seedling
6%
Callus
41%
Root
13%
Pericarp
1%
Pedicel
0.4%
Meristem
2%
Leaf
8%
Ear Shoot
3%
Ear (Cob)
3%
Kernel
1%
Endosperm
3%
Embryo
3%

**Figure 4.**

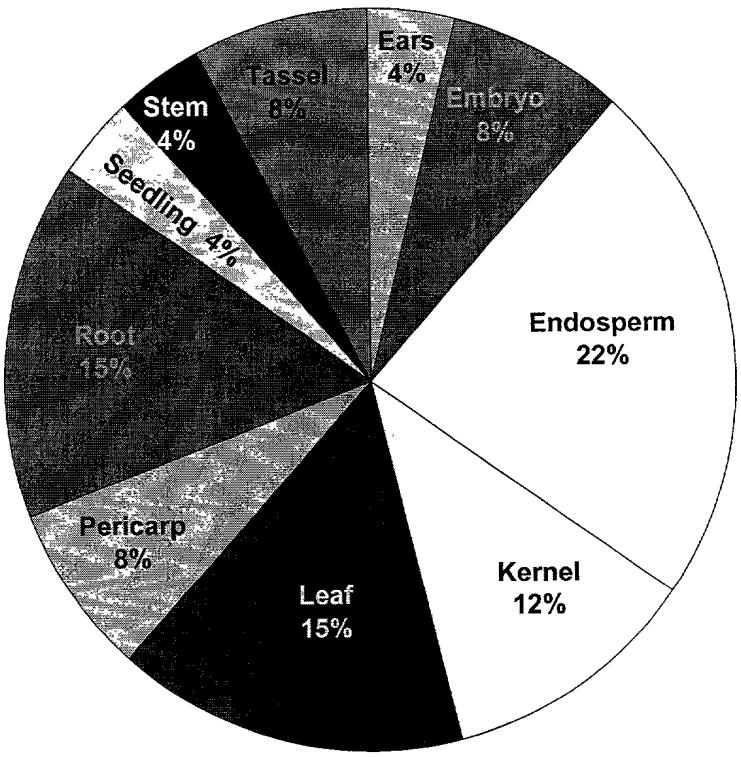



**Figure 5**

EP 0 824 148 B1

Allele 1: CACCCGG-mu-AGATTG

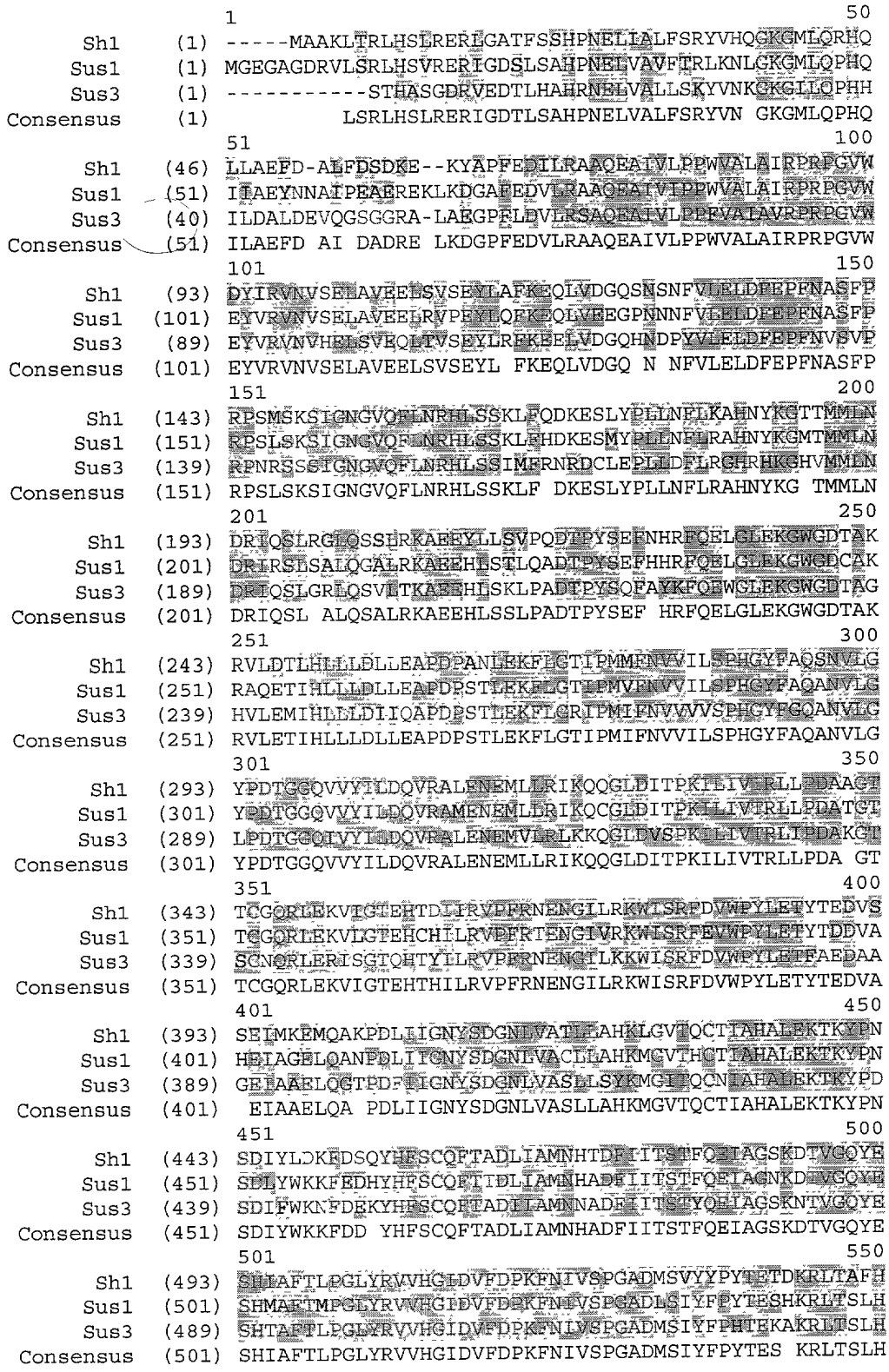
Allele 2: CACC-mu-CGGAGATTG

**Figure 6.**

**Figure 7.**

| Genotype | structural dry matter (% of total dry matter) | cellulose (% of total dry matter) | cellulose (% of structural dry matter) |
|---|---|---|---|
| *Sus-1* (WT) | 63.2 | 25.2 +/-0.38 | 39.9 |
| *sus-1* (mutant) | 47 3 | 17.7 +/-0.34 | 37.4 |

20120704 074305




Docket No.: 0525-4002

**Figure 8a**

```
                    551                                                 600
      Sh1   (543) PEIEELIYSDVENSEHKFVLKDKKKPIIESMARLDRVKNMTGLVEMYGKN
      Sus1  (551) PEIEELLYSQTENTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRN
      Sus3  (539) GSIENLIYDPEQNDEHIGHLDDRSKPILFSMARLDRVKNITGLVEAFAKC
Consensus   (551) PEIEELIYS  ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGKN


                    601                                                 650
      Sh1   (593) ARERELANLVIVAGDHGK-ESKDREEQAEFKKMYSLIDEYKLKGHIRWIS
      Sus1  (601) KRLQELVNLVVVCGDHGN-PSKDKEEQAEFKKMFDLIEQYNLNGHIRWIS
      Sus3  (589) AKLRELVNLVVVAGYNDVNKSKDREEIAEIEKMHELIKTHNLFGQFRWIS
Consensus   (601) ARLRELVNLVVVAGDHG   SKDREEQAEFKKMHDLID YNL GHIRWIS
                    651                                                 700
      Sh1   (642) AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVIESMTCGLPTIATCH
      Sus1  (650) AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATAY
      Sus3  (639) AQTNRARNGELYRYIADTHGAFVQPALYEAFGLTVVEAMTCGLPTFATLH
Consensus   (651) AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFAT H
                    701                                                 750
      Sh1   (692) GGPAEIIVDGVSGLHIDPYHSDKAADILVNFFDKCKADPSYWDEISQGGL
      Sus1  (700) GGPAHIIVHGVSGYHIDPYQGDKASALLVDFFDKCQAEPSHWSKISQGGL
      Sus3  (689) GGPAEIIEHGVSGFHIDPYHPEQAVNLMADFFDRCKQDPDHWVNISGAGL
Consensus   (701) GGPAEIIVHGVSGFHIDPYH DKAA LLVDFFDKCKADPSHW  ISQGGL
                    751                                                 800
      Sh1   (742) QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYIEMFYALKYR
      Sus1  (750) QRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYR
      Sus3  (739) QRIYEKYTWKIYSERLMTLAGVYGFWKYVSKLERLETRRYLEMFYILKFR
Consensus   (751) QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR
                    801           817
      Sh1   (792) SLASQVPLSFD------
      Sus1  (800) TMASTVPLAVEGEPSSK
      Sus3  (789) ELAKTVPLAID-QPQ--
Consensus   (801) SLASTVPLAID  P
```

**Figure 8b**

20040147601

US 2004/0244074 A1 Dec. 2, 2004

```
                1                                                    50
Sh1       (1)   AAACCCTCCCTCCCTCCTCCATTGGACTGCTTGCTCCCTGTTGACCATTG
Sus1      (1)   ----------------------GCCTGAG-GATCCAGGAAGAGGACAG
Sus3      (1)   --------------------------------------------------
Consensus (1)                          G CTG   G TCC  G  GA  A  G
               51                                                   100
Sh1      (51)   GGTATTCTGAACCATCGAGCCATGGCTGCCAAGCTGACTCGCCTTCACAG
Sus1     (26)   CA-ATGGGGGAAGGTGCAGGTGACCGTGTC---CTGAGCCGCCTCCACAG
Sus3      (1)   -----------------------------------GTCGAC-CCACGC
Consensus (51)     AT   G A   T  AG       TG C   CTGAGTCGCCTCCACAG
              101                                                   150
Sh1     (101)   TCTTCGCGAACGCCTTGGTGCCACCTTCTCCTCCCATCGCAATGAACTGA
Sus1     (72)   CGTCAGGGAGCGCATTGGCGAGTCACTCTCTGCCCACCCCAATGAGCTTG
Sus3     (13)   GTCGGCGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGCTCG
Consensus(101)    TC GCGA CGC TTGG GACACCCTCTCCGCCCACCCCAATGAGCT G
              151                                                   200
Sh1     (151)   TAGCACTCTTTTCCAGGTATGTTCACCAGGGCAAGGGAATGCTTCAGCGC
Sus1    (122)   TCGCGGTCTTCACCAGGCTGAAAAACCTTGGAAAGGCTATGCTGCAGCCC
Sus3     (63)   TCGCCCTCCTGTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCG
Consensus(151)  TCGCCCTCTT TCCAGGTA GT AACCAGGG AAGGG ATGCTGCAGCCC
              201                                                   250
Sh1     (201)   CATCAGCTGCTTGCGGAGTTTGA---TGC----CCTGTT--TGATAGTGA
Sus1    (172)   CACCAGATCATTGCCGACTACAACAATGCGATCCCTGAGGCTGAGCGCGA
Sus3    (113)   CACCACATCCTCGACGCCTCGACGAGGT----CCAGGG-CTCCGGGGGC
Consensus(201)  CACCAGATCCTTGCCGAGTTCGAC ATGC    CCTG G CTGAG G GA

              251                                                   300
Sh1     (242)   CAAGGAGAAG--TATGCACCATTTGAAGACATTCTTCGTGCTGCTCAGGA
Sus1    (222)   GAAGCTCAAG--GATCGTGGTTTTGAGCATGTCCTGAGGGCAGCTCAGCA
Sus3    (158)   CGCCGCGCTAGCCCAGGGACCCTTCCTCGACGTGCTCCGCTCCGCGCACGA
Consensus(251)  CAAGC CAAG  GATGGACC TTTGA GACGTCCT CG GC GCTCAGGA
              301                                                   350
Sh1     (290)   ACCAATTGTGCTCCCCCCATGGGTTGCACTTGCTATCAGGCCAAGGCCTG
Sus1    (270)   GCCGATTGTCATCCCCCCATGGGTTGCACTTGCCATCCGCCCTAGGCCTG
Sus3    (208)   GGCGATCGTGCTGCCGCCGTTCGTGGCCATCGCGGTGCGCCCGCGCCCGG
Consensus(301)  GGCGATTGTGCTCCCCCCATGGGTTGCACTTGC ATCCGCCC AGGCCTG
              351                                                   400
Sh1     (340)   GTGTCTGGGATTAGATTCGGGTGAATGTAAGTGAGCTGGCTGTGCAGGAG
Sus1    (320)   GTGTCTCGGAGTATGTGAGGGTCAACGTCAGTGAGCTCGCTGTTGAGGAG
Sus3    (258)   GAGTTTGGGAGTACGTCCGCGTCAACGTTCACGAGCTCAGCGTCCGAGCAG
Consensus(351)  GTGTCTGGGAGTACGT CGGGTCAACGT AGTGAGCTCGCTGT GAGGAG
              401                                                   450
Sh1     (390)   CTGAGTGTTTCTGAGTACTTGGCATTCAAGGAACAGCTGCTGGATGGACA
Sus1    (370)   GTGAGAGTTCCTGAGTACCTGCAGTTCAAGGAACAGCTTGTGCAATAAGG
Sus3    (308)   GTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTTGTCGACGGCCA
Consensus(401)  CTGAGAGTTTCTGAGTACCTGC  TTCAAGGAACAGCTTGTGGA GGACA
              451                                                   500
Sh1     (440)   ATCCAACAGCAACTTTGTGCTTGAGCTTGATTTTGAGCCCTTCAATGCCT
Sus1    (420)   CCCCAACAACAACTTTGTTCTTGAGCTGGACTTTGAGCCATTCAATGCCT
Sus3    (358)   GCACAATGATCCCTACGTTCTTCGAGCTTGACTTCGAGCCGTTCAATGTCT
Consensus(451)   CCCAACAACAACTTTGTTCTTGAGCTTGACTTTGAGCC TTCAATGCCT
              501                                                   550
Sh1     (490)   CCTTTCCTCGTCGTTCCATGTCGAAGTCCATCGGAAATGGAGTGCAATTC
Sus1    (470)   CCTTCCCCCGTCCTTCTCTGTCAAAGTCCATTGGCAATGGCGTGCAGTTC
Sus3    (408)   CAGTCCCACGCCCAAATCGGTCATCATCTATTGGAAACGGTGTGCAGTTC
Consensus(501)  CCTTCCC CGTCCTTCTCTGTCAAAGTCCATTGGAAATGG GTGCAGTTC
```

**Figure 9a**

4,908,474 - 05/13/90

```
                    551                                                 600
Sh1          (540)  CTTAACCGACACCTGTCGTCCAAGTTGTTCCAGGACAAGGAGAGTTTGTA
Sus1         (520)  CTCAACAGGCACCTGTCATCAAAGCTCTTCCATGACAAGGAGAGCATGTA
Sus3         (458)  CTCAAGCGACACTTGTCCTCAATCATGTTCCGCAACAGGGATTGCTTGGA
Consensus    (551)  CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGAGAGCTTGTA
                    601                                                 650
Sh1          (590)  CCCCTTGCTGAACTTCCTCAAGGCTCATAACTACAAGCGCACGACGATGA
Sus1         (570)  CCCCTTGCTCAACTTCCTTCGCGCCCACAACTACAAGCGGATGACCATGA
Sus3         (508)  GCCCCTGTTGGATTTCCTCCGTGGCCACCGGCACAAGCGGCATGTTATGA
Consensus    (601)  CCCCTTGCTGAACTTCCTCCG GCCCACAACTACAAGGGGA GAC ATGA
                    651                                                 700
Sh1          (640)  TGTTGAATGACAGAATCCAAAGCCTTCGTGGTCTCCAATCATCCCTGAGA
Sus1         (620)  TGTTGAACGACAGAATCCGCAGTCTCAGTGCTCTGCAAGGTGCGCTGAGG
Sus3         (558)  TGCTTAATGATAGAATACAAAGCTTGGGGAGGCTTCAGTCTGTGCTCACC
Consensus    (651)  TGTTGAATGACAGAATCCAAAGCCT  GTGGTCT CAATCTGCGCTGAG
                    701                                                 750
Sh1          (690)  AAGGCAGAGGAGTATCTACTGAGTGTTCCTCAAGACACTCCCTACTCGGA
Sus1         (670)  AAGCCTGAGGAGCCACCTGTCCACCCTACAAGCTGATACCCCATACTCTGA
Sus3         (608)  AAAGCTGAGCACCACTTGTCAAAGCTCCCTGCTGACACACCATACTCACA
Consensus    (701)  AAGGCTGAGGAGCACCTGTC A  CT CCTGCTGACAC CCATACTC GA
                    751                                                 800
Sh1          (740)  GTTCAACCATAGGTTCCAAGAGCTTGGCTTGGAGAAGGGTTGGGGTGACA
Sus1         (720)  ATTTCACCACAGGTTCCAGGAACTTCGTCTCGGAGAAGCGTTGCGGTGATT
Sus3         (658)  ATTTGCTTATAAATTTCAAGAGTGGGCGCTGGAGAAAGCTTCGGGTCATA
Consensus    (751)  ATTT ACCATAGGTTCCAAGAGCTTGGCCTGGAGAAGGGTTGGGGTGATA
                    801                                                 850
Sh1          (790)  CTGCGAAGCGTGTTCTCGACACACTCCACTTGCTTCTCGACCTTCTTGAG
Sus1         (770)  GCGCTAAGCGTGCACAGGAGACTATCCACCTCCTCTTGGACCTCCTGGAG
Sus3         (708)  CAGCAGGACATGTTTTGGAAATGATCCATCTCCTTCTAGACATCATTCAG
Consensus    (801)  C GC AAGCGTGTTCTGGA AC ATCCACCTCCTTCT GACCTCCTTGAG
                    851                                                 900
Sh1          (840)  GCCCGTGATCCTGCCAACTTGGAGAAGTTCCTTGGAACTATACGAATGAT
Sus1         (820)  GCCCCAGATCCGTCCACCCTGGAGAAGTTCCTTGGAACGATGCCCATGGT
Sus3         (758)  GCGCCAGACCCATCTACCGTAGAGAAATTGTTGGCGAGGATGCCCATGAT
Consensus    (851)  GCCCCAGATCC TCCACCCTGGAGAAGTTCCTTGGAACGATCCCCATGAT
                    901                                                 950
Sh1          (890)  GTTCAACGTTGTTATCCTGTGTCCTCATGGCTACTTGGCCCAGTCCAATG
Sus1         (870)  GTTCAATGTCGTTATCCTCTCCGCTCATGGTTACTTCGCTCAAGCTAATG
Sus3         (808)  TTTTAACGTTGTTGTGGTATCCCCTCATGGATACTTTGGTCAAGCTAATG
Consensus    (901)  GTTCAACGTTGTTATCCT TCCCCTCATGG TACTTCGCTCAAGCTAATG
                    951                                                1000
Sh1          (940)  TGCTTGGATACCCTCACACTGGCGGTCAGGTTGTGTACATTCTGGATCAA
Sus1         (920)  TCTTGCGTTACCCTGACACCGGAGGCCAGGTTGTCTACATCTTGGATCAA
Sus3         (858)  TATTAGGCTTGTCCAGACACAGCAGGACAGATCGTCTATATACTGGACCAA
Consensus    (951)  T TT GG TACCCTGACAC GGAGG CAGGTTGTCTACAT CTGGATCAA
                    1001                                               1050
Sh1          (990)  GTCCGTGCTTTGGAGAATGAGATGCTTCTGAGGATTAAGCAGCAAGGCCT
Sus1         (970)  GTGCGCGCTATGGAGAACGAAATGCTGCTGAGGATCAAGCAGTGTGGTCT
Sus3         (908)  GTCCGTGCACTACAAAATGAGATGGTTCTCCGTTTAAAGAAACAAGGGCT
Consensus   (1001)  GTCCGTGCT TGGAGAATGAGATGCTTCTGAGGAT AAGCAGCAAGG CT
                    1051                                               1100
Sh1          (1040) TGATATCACTCCGAAGATGCTCATTGTTACCAGGCTGTTGCCTGATGCTG
Sus1         (1020) TGACATCACGCCGAAGATCCTTATTGTCACCAGGTTGCTCCCTGATGCAA
Sus3          (958) TGATGTTTCCCCAAAGATTCTCATTGTTACTCGGCTGATACCAGATGCAA
Consensus   (1051)  TGATATCAC CCGAAGATCCTCATTGTTACCAGGCTG T CCTGATGCAA
```

**Figure 9b**

3015230.4.1.20050704

```
                    1101                                                1150
      Sh1   (1090) CTGGCACTACGTCCGGTCAGCCGCTGCAGAAGGTCATTGGTACTGAGCAC
      Sus1  (1070) CTGGCACCAGCTGTGGCCAGCGCGTTGAGAAGGTCCTTGGCACCGAGCAC
      Sus3  (1008) AAGGAACATCATGCAATCAGCGGCTTGAGAGAATTAGTGGAACACAGCAT
Consensus   (1101) CTGG AC AC TGCGGTCAGCGGCTTGAGAAGGTCATTGG AC GAGCAC
                    1151                                                1200
      Sh1   (1140) ACAGACATCATTCGCGTTCCCTTCAGAAATGAGAATGGCATCCTCCGCAA
      Sus1  (1120) TGCCATATCCCTCGCGTGCCATTGAGAACAGAAAACGGAATCGTTCGCAA
      Sus3  (1058) ACTTACATATTACGAGTTCCCTTCAGAAATGAAAATGGGATACTTAAGAA
Consensus   (1151) AC  ACATC TTCGCGTTCCCTTCAGAAATGAAAATGG ATCCTTCGCAA
                    1201                                                1250
      Sh1   (1190) GTGGATCTCTCGTTTTGATGTCTGGCCATACCTGGAGACATACACTGAGG
      Sus1  (1170) GTGGATCTCGCCATTTGAAGTCTGGCCGTACCTGGAGACTTACACTGATG
      Sus3  (1108) ATGGATATCAAGATTTGATGTGTGGCCATATCTGGAAACATTTGCTGAGG
Consensus   (1201) GTGGATCTC CGATTTGATGTCTGGCCATACCTGGAGACATACACTGAGG
                    1251                                                1300
      Sh1   (1240) ATGTTTCCAGTGAAATAATGAAACAAATGCAGGGCAAGGCTGACCTTATC
      Sus1  (1220) ACGTGGCGCATGAGATTGCTGGAGAGCTTCAGGCCAATCCTGACCTGATC
      Sus3  (1158) ATGCTGCTGGTGAAATTGCTGCTCAATTACAAGGTACTCCAGACTTCATA
Consensus   (1251) ATGTTGC  GTGAAATTGCTG AGAA T CAGGCCAATCCTGACCT ATC
                    1301                                                1350
      Sh1   (1290) ATTGGCAACTACAGCGATGGCAACCTAGTCGGCACTCTGCTCGGCGCACAA
      Sus1  (1270) ATCGCAAACTACAGTGACGGAAACCTTGTTGCGTGTTTGCTCGCCCACAA
      Sus3  (1208) ATTGCAAACTACAGTGATGGAAATCTTGTGGCGTCATTGCTATCTTACAA
Consensus   (1301) ATTGGAAACTACAGTGATGGAAACCTTGT GCGTCTTTGCTCGC CACAA
                    1351                                                1400
      Sh1   (1340) GTTGGGAGTCACTCAGTGTACCATCGCTCATGCCTTGGAGAAAACCAAAT
      Sus1  (1320) CATGGCTGTTACTCACTGTACCATTGCCCATGCGCTTCAGAAAACTAAGT
      Sus3  (1258) GATGCCAATTACCCAGTGCAACATTGCTCATGCTCTGCAAAAGACTAAGT
Consensus   (1351) GATGGGAGTTACTCAGTGTACCATTGCTCATGC CTGGAGAAAACTAAGT
                    1401                                                1450
      Sh1   (1390) AGCCCAACTCGGACATCTACTTGGACAAATTCGACAGCCAGTACCACTTC
      Sus1  (1370) ACCCTAACTCCGACCTCTACTGCAAGAAGTTTGAGGATCACTACCACTTC
      Sus3  (1308) ATCCAGATTCAGACATATTTTGCAAGAATTCCATGAGAAGTACCATTTC
Consensus   (1401) ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC
                    1451                                                1500
      Sh1   (1440) TCTTGCCAGTTCACAGCTGACCTTATTGCCATGAACCACACCGATTTCAT
      Sus1  (1420) TCGTGCCAGTTGACCACTGACTTGATTGCAATGAACCATGCCGACTTCAT
      Sus3  (1358) TCCTGCCAGTTCACTGCTGATATAATTGCTATGAACAATGCTGATTTTAT
Consensus   (1451) TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCGATTTCAT
                    1501                                                1550
      Sh1   (1490) CATCACCAGCACATTCCAAGAAATCGCGGAAGCAAGGACACCGTGGGGC
      Sus1  (1470) CATCACCAGTAGCTTCCAAGAGATCGCCGGAAACAAGGACACCGTCGGCC
      Sus3  (1408) CATCACCACCACATACCAAGAAATTGCTGGAAGCAAAAATAGTGTTGGAC
Consensus   (1501) CATCACCAGCACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C
                    1551                                                1600
      Sh1   (1540) AGTACGAGTCCCATATCGCGTTCACTCTTGCTGGGCTCTACCGTGTCGTC
      Sus1  (1520) AGTACGAGTCACACATGGCGTTCACAATGCCTGGCCTGTACCGCGTTGTC
      Sus3  (1458) AGTATGAGAGTCATACTGCCTTTACTCTGCCTGGTCTGTACCGAGTTGTC
Consensus   (1551) AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTTGTC
                    1601                                                1650
      Sh1   (1590) CATGGCATCGATGTTTTCGATCCCAAGTTCAACATTGTCTCTCCTGGAGC
      Sus1  (1570) CACGGCATTGATCTGTTCGACCCCAAGTTCAACATCGTGTCTCCTGGCGC
      Sus3  (1508) CATGGGATCGATGTCTTCGATCCAAAGTTCAATATAGTCTCTCCTGGAGC
Consensus   (1601) CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCCTGGAGC
```

**Figure 9c**

20120244-1700004

```
                    1651                                                1700
      Sh1   (1640) AGACATGAGTGTTTACTACCCTTATACGGAAACCGACAAGAGACTCACTG
      Sus1  (1620) GGACCTGTGCCATCTACTTCCCGTACACCGAGTCGCACAAGAGGCTGACCT
      Sus3  (1558) TGACATGTCCATATACTTTCCACATACCGAGAAGGCCAAGCGACTCACCT
Consensus   (1651)  GACATGTCCAT TACTTCCC TATACCGAGACGGACAAGAGACTCACCT

                    1701                                                1750
      Sh1   (1690) CCTTCCATCCTGAAATCGAGGAGCTCATCTACAGCGACGTCGAGAAGTCC
      Sus1  (1670) CCCTTCACCCGCAGATTGAGGAGCTCCTGTAGAGCCAAACGGAGAACACG
      Sus3  (1608) CTCTTCATGGTTCAATCGAAAATTTGATTTATGACCCGCAGCAAAACGAT
Consensus   (1701) CCCTTCATCCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C
                    1751                                                1800
      Sh1   (1740) GAGCACAAGTTCGTGCTGAAGGACAAGAAGAAGCCGATCATCTTCTCGAT
      Sus1  (1720) GAGCACAAGTTCGTTCTCAACGACAGGAACAAGCCAATCATCTTCTCCAT
      Sus3  (1658) CAACACATTGGGCATCTGGATGACCGGTCAAAGCCCATCCTCTTCTCCAT
Consensus   (1751) GAGCACAAGTTCGTTCTGAA GACAGGAA AAGCC ATCATCTTCTCCAT
                    1801                                                1850
      Sh1   (1790) GGCGCGTCTCGACCGCGTGAAGAACATGACAGGCCTGGTCGAGATGTACG
      Sus1  (1770) GGCTCGTCTCGACCGTGTGAAGAACTTGACTGGGCTGGTGCAGCTGTACG
      Sus3  (1708) GGCAAGACTCGACAGGGTGAAGAACATAACACGGCTGGTCGAAGCTTTTG
Consensus   (1801) GGC CGTCTCGACCG GTGAAGAACATGACAGGGCTGGTCGAG TGTACG
                    1851                                                1900
      Sh1   (1840) GCAACAACGCGCGCCTGAGGGAGCTGGCGAACCTCGTGATCGTTGCCGGT
      Sus1  (1820) GCCGGAACAAGCGGCTGCAGGAGCTGGTGAACCTCGTGGTCGTCTGCGGC
      Sus3  (1758) CTAAGTGCGCTAAGCTGAGGCAGCTGGTAAACCTTGTCGTCGTTGCCGGG
Consensus   (1851) GCAAGAACGCGCGGCTGAGGGAGCTGGTGAACCTCGTGGTCGTTGCCGG
                    1901                                                1950
      Sh1   (1890) GACCACGG---CAAGGAGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA
      Sus1  (1870) GACCATGG---CAACCCTTCGAACGACAAGGAGGAGCAGGCGGAGTTCAA
      Sus3  (1808) TACAATGATGTCAACAAGTCCAAGGACAGGGAAGAGATCGCGGAGATAGA
Consensus   (1901) GACCATGG   CAAC AGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA
                    1951                                                2000
      Sh1   (1937) GAAGATGTACAGCCTCATCGACGAGTACAAGTTCAAGGGCCATATCCGGT
      Sus1  (1917) GAAGATGTTTGACCTCATCGAGCAGTACAACCTGAACGGGCACATCCGCT
      Sus3  (1858) GAAGATGCATGAACTCATCAAGACCCACAACTTGTTCGGGCAGTTCCGCT
Consensus   (1951) GAAGATGTATGACCTCATCGAG AGTACAACTTGAACGGGCA ATCCGCT
                    2001                                                2050
      Sh1   (1987) GGATCTCGGCGCAGATCAACCGTGTCCGCAACGGCGAGCTGTACCGCTAC
      Sus1  (1967) GGATCTCCGCCCAGATGAACCGCGTGCGCAACGGCGAGCTGTACCGCTAC
      Sus3  (1908) GGATCTCTGCGCAGACAAACAGGGCCCGTAACGGCGAGCTCTATCGCTAC
Consensus   (2001) GGATCTC GCCCAGATGAACCG GTCCGCAACGGCGAGCTGTACCGCTAC

                    2051                                                2100
      Sh1   (2037) ATTTGCGATACCAAGGGCGCATTCGTGCAGCCTGCGTTCTACGAAGCGTT
      Sus1  (2017) ATCTGCGACACCAAGGGCGCCTTCGTGCAGCCTGCTTTCTACGAGGCTTT
      Sus3  (1958) ATCGCTGATACCCATCGTGCTTTCGTACAGCCGGCCTTGTATGAAGCGTT
Consensus   (2051) ATCTGCGATACCAAGGGCGC TTCGTGCAGCCTGC TTCTACGAAGCGTT
                    2101                                                2150
      Sh1   (2087) CGGCCTGAGTGTGATCCAGTCCATGACGTGCGGTCTGCCAACGATCGCGA
      Sus1  (2067) CGGGCTGACGGTGGTTCAGGCGATGACCTGCGGCCTGCCCACGTTCGCCA
      Sus3  (2008) CGGTCTCACCGTCGTTGAGGCCATGACCTGTGGGCTTCCTACTTTCGCGA
Consensus   (2101) CGG CTGAC GTGGTTGAGGCCATGACCTGCGG CTGCC ACGTTCGCGA
                    2151                                                2200
      Sh1   (2137) CCTGCCATGGCCGCCCTGCTGAGATCATCGTGGACGGGGTATCTGGCCTG
      Sus1  (2117) CCGCCTACCGCGGTCCGGCCGAGATCATCGTGCACGGCGTGTCTGGCTAC
      Sus3  (2058) CGCTCCATCGAGGTCCAGCTGAGATCATACAGCATGGCGTCTCGGGCTTC
Consensus   (2151) CC  CCATGGCGGTCC GCTGAGATCATCGTGCACGGCGT TCTGGCTTC
```

**Figure 9d**

4000044 - 020204

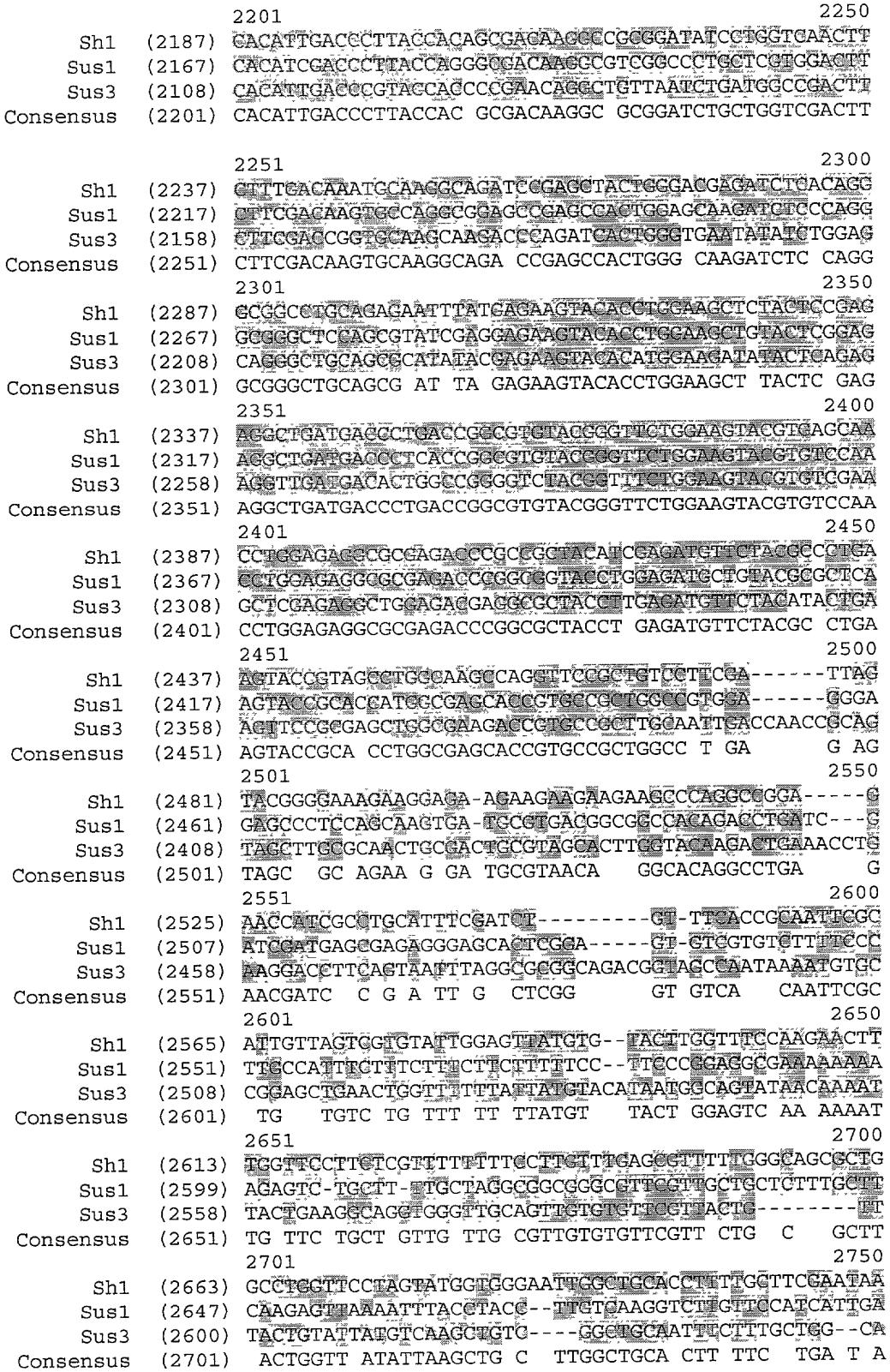



**Figure 9e**

```
                  2751                                                2800
      Sh1   (2713) AAATGCCTGCTCGTTCACCTGTCTTCCAGAGTGC----------------
      Sus1  (2695) TCCGGGTGTCGCTTGTAGTAGTCTGATGCACTGTTAGTAGTTTGCGTTGC
      Sus3  (2644) AGCCGCAGGCACTGGTGAAGTGCTGATAAATACATCATATTCTGTTGACC
Consensus   (2751) A C GC GGC CTTGTA   GTCTGATAGA TG T  TA T TG     C
                  2801                                                2850
      Sh1   (2747) ----------------------------------------------------
      Sus1  (2745) GTCGGTTGAGAGGGAACGTTGGTGGTGGTGGTGTGTGTGCAGTCAGGCGT
      Sus3  (2694) TGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC------
Consensus   (2801)    G    A A   AA                  G G G    C

                  2851                                                2900
      Sh1   (2747) ----------------------------------------------------
      Sus1  (2795) GGTGCTCCCTTTGTTTCCTGGATGGGATGTTGCTCCTTGAATAATAATCG
      Sus3  (2738) ----------------------------------------------------
Consensus   (2851)
                  2901                                                2950
      Sh1   (2747) ----------------------------------------------------
      Sus1  (2845) TAGTGGCCTTGGAGCCCTTTTCCTGAAATAAGAGCAGCATCCTAGTGCTT
      Sus3  (2738) ----------------------------------------------------
Consensus   (2901)
                  2951      2964
      Sh1   (2747) --------------
      Sus1  (2895) ACCTTTGCAGCTGT
      Sus3  (2738) --------------
Consensus   (2951)
```

**Figure 9f**

EP 1 284 294 A2 20030219

CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGCGGCCGCGGGTAGGAG

CGCGCGCGGCGCGGCGGAACGACCCACCGGTGGCGGCAGCC**ATG**TCTGCCCCGAAGCTGA

ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC

TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA

TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCT

TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

**Figure 10**

EP 1 894 949 A2 - 05-03-2008

## Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11

ATGTCTGCCCCGAAGCTGAACCGCAACGCGAGCATCCGG

## Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

gtcgaccccac gcgtccgggcg accgcgtcga ggacaccctc cacgcgcacc gcaacgagct 60
cgtcgccctc ctgtccaagt acgtgaacaa ggggaagggc atcctgcagc cgcaccacat 120
cctcgacgcg ctcgacgagg tccagggctc cgggggccgc gcgctagccg agggacccct 180
cctcgacgtc ctccgctccg cgcaggaggc gatcgtgctg ccgccgttcg tggccatcgc 240
ggtgcgcccg cgcccgggag tttgggagta cgtccgcgtc aacgttcacg agctcagcgt 300
cgagcagctc acagtctcgg agtacctccg cttcaaggag gagcttgtcg acggccagca 360
caatgatccc tacgttctcg agcttgactt cgagccgttc aatgtctcag tcccacgccc 420
aaatcggtca tcatctattg gaaacggtgt gcagttcctc aaccgacact tgtcctcaat 480
catgttccgc aacagggatt gcttggagcc cctgttggat ttcctccgtg gccaccggca 540
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gctgaccaaa gctgaggagc acttgtcaaa gctccctgct gacacaccat actcacaatt 660
tgcttataaa tttcaagagt ggggcctgga gaaaggttgg ggtgatacag caggacatgt 720
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gaaattcttg gggaggatcc ccatgatttt taacgttgtt gtggtatccc ctcatggata 840
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cttcataatt ggaaactaca gtgatggaaa tcttgtggcg tcattgctat cttacaagat 1260
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catattttgg aagaatttcg atgagaagta ccatttctcc tgccagttca ctgctgatat 1380
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aaaaaaaaaa aaaaaaaaaa aaaaaaaggg cggccgc

**Figure 11**